

Figure 1
Nucleotide Sequence and predicted protein for HLTDG74

-88	10	30	50	
	GT	TTGCTCTGGGCAGCCAAGTTGGCATATTGGAAGCTTTTCCGGGCTCTGGAGGAGGGT	-29	
-28	70	90	110	31
-8	CCCTGCTTCTTCTACAGCCGTTCCGGGCATGGCCTGGCTGGGGGCGTCGCTCCACGTCT			11
		M A W L G A S L H V W		
32	130	150	170	91
12	GGGGTTGGCTAATGCTCGGCAGCTGCCTCCTGGCCAGAGCCCAGCTGGATTCTGATGGCA			31
	G W L M L G S C L L A R A Q L D S D G T			
92	190	210	230	151
32	CCATCACTATAGAGGAGCAGATTGTCCTTGTGCTGAAAGCGAAAGTACAATGTGAACTCA			51
	I T I E E Q I V L V L K A K V Q C E L N			
152	250	270	290	211
52	ACATCACAGCTCAACTCCAGGAGGGAGAAGGTAATTGTTTCCCTGAATGGGATGGACTCA			71
	I T A Q L Q E G E G N C F P E W D G L I			
212	310	330	350	271
72	TTTGTGGCCAGAGGAACAGTGGGGAAAATATCGGCTGTTCCATGCCCTCCTTATATTT			91
	C W P R G T V G K I S A V P C P P Y I Y			
272	370	390	410	331
92	ATGACTTCAACCATAAAGGAGTTGCTTTCGACACTGTAACCCCAATGGAACATGGGATT			111
	D F N H K G V A F R H C N P N G T W D F			
332	430	450	470	391
112	TTATGCACAGCTTAAATAAAACATGGGCCAATTATTCAGACTGCCTTCGCTTCTGCAGC			131
	M H S L N K T W A N Y S D C L R F L Q P			
392	490	510	530	451
132	CAGATATCAGCATAGGAAAGCAAGAATTCTGTGAACGCCTCTATGTAATGTATACCGTTG			151
	D I S I G K Q E F C E R L Y V M Y T V G			
452	550	570	590	511
152	GCTACTCCATCTCTTTGGTTCCTTGGCTGTGGCTATTCTCATCATTGGTTACTTCAGAC			171
	Y S I S F G S L A V A I L I I G Y F R R			
512	610	630	650	571
172	GATTGCATTGCACTAGGAACTATATCCACATGCACTTATTTGTGTCTTTCATGCTGAGAG			191
	L H C T R N Y I H M H L F V S F M L R A			
572	670	690	710	631
192	CTACAAGCATCTTTGTCAAAGACAGAGTAGTCCATGCTCACATAGGAGTAAAGGAGCTGG			211
	T S I F V K D R V V H A H I G V K E L E			

FIGURE 1 1/3

632	730	750	770	691
212	AGTCCCTAATAATGCAGGATGACCCACAAAATTCATTGAGGCAACTTCTGTGGACAAAT			231
	S L I M Q D D P Q N S I E A T S V D K S			
692	790	810	830	751
232	CACAATATATCGGGTGCAAGATTGCTGTTGTGATGTTTATTTACTTCCTGGCTACAAATT			251
	Q Y I G C K I A V V M F I Y F L A T N Y			
752	850	870	890	811
252	ATTATTGGATCCTGGTGGAAGGTCTCTACCTGCATAATCTCATCTTTGTGGCTTTCTTTT			271
	Y W I L V E G L Y L H N L I F V A F F S			
812	910	930	950	871
272	CGGACACCAAATACCTGTGGGGCTTCATCTTGATAGGCTGGGGGTTTCCAGCAGCATTTG			291
	D T K Y L W G F I L I G W G F P A A F V			
872	970	990	1010	931
292	TTGCAGCATGGGCTGTGGCACGAGCAACTCTGGCTGATGCGAGGTGCTGGGAACCTTAGTG			311
	A A W A V A R A T L A D A R C W E L S A			
932	1030	1050	1070	991
312	CTGGAGACATCAAGTGGATTTATCAAGCACCGATCTTAGCAGCTATTGGGCTGAATTTTA			331
	G D I K W I Y Q A P I L A A I G L N F I			
992	1090	1110	1130	1051
332	TTCTGTTTCTGAATACGGTTAGAGTTCTAGCTACCAAATCTGGGAGACCAATGCAGTTG			351
	L F L N T V R V L A T K I W E T N A V G			
1052	1150	1170	1190	1111
352	GGCATGACACAAGGAAGCAATACAGGAACTGGCCAAATCGACACTGGTCCTGGTCCTAG			371
	H D T R K Q Y R K L A K S T L V L V L V			
1112	1210	1230	1250	1171
372	TCTTTGGAGTGCATTACATCGTGTTCGTGTGCCTGCCTCACTCCTTCACTGGGCTCGGGT			391
	F G V H Y I V F V C L P H S F T G L G W			
1172	1270	1290	1310	1231
392	GGGAGATCCGCATGCACTGTGAGCTCTTCTTCAACTCCTTTCAGGGTTTCTTTGTGTCTA			411
	E I R M H C E L F F N S F Q G F F V S I			
1232	1330	1350	1370	1291
412	TCATCTACTGCTACTGCAATGGAGAGGTTTCAGGCAGAGGTGAAGAAGATGTGGAGTCGGT			431
	I Y C Y C N G E V Q A E V K K M W S R W			
1292	1390	1410	1430	1351
432	GGAATCTCTCCGTGGACTGGAAAAGGACACCGCCATGTGGCAGCCGAGATGCGGCTCAG			451
	N L S V D W K R T P P C G S R R C G S V			
1352	1450	1470	1490	1411
452	TGCTCACCACCGTGACGCACAGCACCAGCAGCCAGTCACAGGTGGCGGCAGCACACGCAT			471
	L T T V T H S T S S Q S Q V A A A H A W			
	1510	1530	1550	

FIGURE 1 2/3

1412 GGTGCTTATCTCTGGCAAAGCTGCCAAGATGCCAGCAGACAGCCTGACAGCCACATCAC 1471
 472 C L S L A K L P R S P A D S L T A T S L 491
 1570 1590 1610
 1472 TTTACCTGGCTATGTCTGGAGTAACTCAGAGCAGGACTGCCTCACACACTCTCTCCACGA 1531
 492 Y L A M S G V T Q S R T A S H T L S T R 511
 1630 1650 1670
 1532 GGAGCAACAAGGAAGATAGTGGGAGGCAGAGAGATGATATTCTAATGGAGAAGCCTTCCA 1591
 512 S N K E D S G R Q R D D I L M E K P S R 531
 1690 1710 1730
 1592 GGCCTATGGAATCTAACCAGACACTGAAGGATGACAAGGAGAACTGAGGATGTTCTCT 1651
 532 P M E S N P D T E G 541
 1750 1770 1790
 1652 GAATGGACATGTGTGGCTGACTTTCATGGGCTGGTCCAATGGCTGGTTGTGTGAGAGGGC 1711
 1810 1830 1850
 1712 TTGGCTGATACTCCTATGCTTGAGCACAAAGGCTGAAAATTCAGTTAAGGTGTTACTTAA 1771
 1870 1890 1910
 1772 TAATAGTTTTTAGGCTCCATGAATTGGCTCCTGTAAATACTAACGACATGAAAATGCAAG 1831
 1930 1950 1970
 1832 TGTCAATGGAGTAGTTTATTACCTTCTATTGGCATCAAGTTTTCTCTAAATTAATGTAT 1891
 1990
 1892 GGTATTTGCTCTGTGATTGTTCA 1914

FIGURE 1 3/3

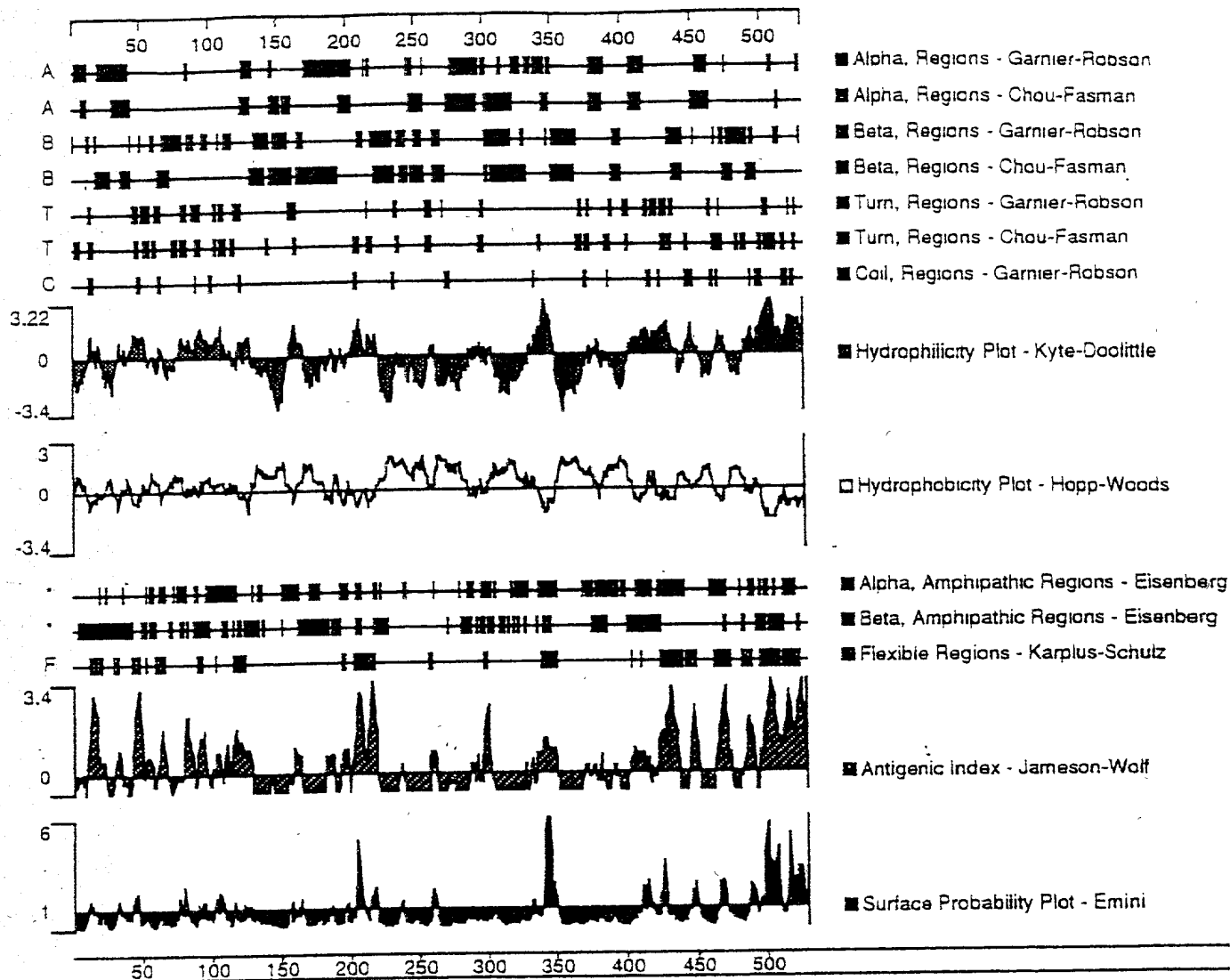


FIGURE 2 1/1

gp M74445 OPOPTHYR_1	parathyroid hormone receptor [Di... +3	597	8.2e-204	6
pir S A39286	parathyroid hormone / parathyroi... +3	597	1.9e-203	6
gp L04308 HUMPTHYR_1	parathyroid hormone receptor [Ho... +3	580	6.7e-190	5
pir S S29610	parathyroid hormone receptor - h... +3	580	6.1e-189	5
gp M77184 RATPATHYR_1	parathyroid hormone receptor [Ra... +3	576	7.7e-188	5
gp X78936 MMPHRPR_1	parathyroid hormone/parathyroid ... +3	576	7.7e-188	5
pir S A42698	parathyroid hormone and parathyr... +3	576	7.7e-188	5
gp L34611 MUSPTHYR06_1	parathyroid hormone/parathyroid ... +3	576	4.1e-174	5
gp U11087 HSV1RG9_1	vasoactive intestinal peptide 1 ... +3	319	1.2e-98	5
gp M86835 RATVASREC_1	vasoactive intestinal polypeptid... +3	254	3.1e-91	5

FIGURE 3

-G- W+++M + FNSFQGFFV+IIYC+QNGEVQAE+KK WS L++D-KF GS
Sbjct: 427 SGILWQVQMHyLMLFNSFQGFFV+IIYCFQNGEVQAEIKKSWL LALDFKRRKARSGS 485

Score = 72 (33.1 bits), Expect = $8.2e-204$, Sum P(6) = $8.2e-204$
Identities = 16/37 (43%), Positives = 23/37 (62%), Frame = +3

Query: 159 AQLDS DGTITIEEQIVLV LKAKVQCELNIT AQLQEGE 269
A +D+D IT EEQI+L+ A+ QCE + L+ E
Sbjct: 24 ALVDADDVITKEEQIILLRNAQAQCEQRLKEVLRVPE 60

Score = 39 (17.9 bits), Expect = $8.2e-204$, Sum P(6) = $8.2e-204$
Identities = 9/23 (39%), Positives = 12/23 (52%), Frame = +2

Query: 1508 ISGKAAKIASRQPD SHITLPGYV 1576
+S + A A + H LPGYV
Sbjct: 512 LSPRLAPGAGASANGHHQLPGYV 534

FIGURE 3